Amendments to the Specification:

Please replace the paragraph beginning at page 5, line 29, with the following:

--According to another aspect, the monomeric analogue is the INSL3 analogue designated ~~eINSLa~~ cINSL3a in Figure 3.--

Please replace the paragraph beginning at page 6, line 1, with the following:

--In a further aspect, the monomeric analogue is the INSL3 analogue designated ~~eINSLb~~ cINSL3b in Figure 3.--

Please replace the paragraph beginning at page 7, line 17, with the following:

--In a preferred form, the method produces the INSL3 analogue designated ~~eINSLa~~ cINSL3a in Figure 3.--

Please replace the paragraph beginning at page 7, line 20, with the following:

--In another preferred form, the method produces the INSL3 analogue designated ~~eINSLb~~ cINSL3b in Figure 3.--

Please replace the paragraph beginning at page 10, line 4, with the following:

--FIGURE 1: Schematic representation of bindingof INSL3, ~~eINSLa~~ cINSL3a and ~~eINSLb~~ cINSL3b analogues to the LGR8 receptor.--

Please replace the paragraph beginning at page 10, line 7, with the following:

--FIGURE 3: Sequences and constraints of the native relaxin (SEQ ID NO:2) and ~~INSL3 B chains~~ INSL3 B-chains (SEQ ID NO:7) with exemplary analogues (SEQ ID NOS:11-13) designed.--

Please replace the paragraph beginning at page 10, line 13, with the following:

--FIGURE 4: Schematic representation of antagonistic activity of ~~eINSLa~~ cINSL3a in the inhibition of the response of INSL3 (measured by cAMP response) to the native INSL3 receptor (LGR8).--

Please replace the paragraph beginning at page 10, line 17, with the following:

--FIGURE 5: Schematic representation illustrating CD spectra of ~~eINSLa~~ cINSL3a showing significant alpha-helical content in water and phosphate buffered saline.--

Please replace the paragraph beginning at page 12, line 15, with the following:

--In a particularly preferred aspect, the B-chain peptide analogue is the INSL3 analogue designated ~~eINSLa~~ cINSL3a in Figure 3.--

Please replace the paragraph beginning at page 12, line 18, with the following:

--In yet another preferred form, the B-chain peptide analogue is the INSL3 analogue designated ~~eINSLb~~ cINSL3b in Figure 3.--

Please replace the paragraph (**TABLE A**) beginning at page 15, line 15, with the following:

--TABLE A

CONSERVATIVE SUBSTITUTIONS I

Side Chain Characteristic	Amino Acid
Aliphatic non-polar	~~G A P I L V~~ G, A, P, I, L, V
Polar — uncharged	~~C S T M N Q~~ C, S, T, M, N, Q
Polar — charged	~~D E K R~~ D, E, K, R
Aromatic	~~H F W Y~~ H, F, W, Y
Other	~~N Q D E~~ N, Q, D, E

--

Please replace the paragraph (**TABLE B**) beginning at page 15, line 26, with the following:

--TABLE B

CONSERVATIVE SUBSTITUTIONS II

Side Chain Characteristic	Amino Acid
Non-polar (hydrophobic)	
A. Aliphatic:	~~A L I V P~~ A, L, I, V, P
B. Aromatic:	~~F W~~ F, W
C. Sulphur-containing:	M
D. Borderline:	G
Uncharged-polar	
A. Hydroxyl:	~~S T Y~~ S, T, Y
B. Amides:	~~N Q~~ N, Q
C. Sulfhydryl:	C
D. Borderline:	G
E. Positively Charged (Basic):	~~K R H~~ K, R, H
F. Negatively Carged (Acidic):	~~D E~~ D, E

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Please replace the paragraph beginning at page 23, line 6, with the following:

--Using SYBYL molecular modelling software (Tripos) on a Silicon Graphics O2 workstation, we designed a model of INSL3 B-chain from the X-ray crystal structure of human Gene 2 relaxin B-chain as a template (Eigenbrot *et al.*,1991, *J Mol Biol* 221: 15-21). After modifying the sequence to resemble that of INSL3, an energy minimisation using a Tripos forcefield with Gasteiger-Marsili charges was carried out. From the resulting energy minimised model, two residues were identified (Glu^4 and Arg^{26}) to have Cβ atoms within 4Å of each other.

These residues were then replaced with cysteine and a disulphide bond formed to give the cyclic peptide ~~cINSLa~~ cINSL3a.--

Please replace the paragraph beginning at page 23, line 15, with the following:

--A second cyclic analogue ~~cINSLb~~ cINSL3b was formed by changing His^{12} to Arg, to mimic a relaxin-like binding motif of Arg-X-X-Arg-X-X-X-Val.--

Please replace the paragraph beginning at page 25, line 27, with the following:

--Following the biological characterisation of peptides cRlx and ~~cINSLa~~ cINSL3a (Figure 3), an additional compound was prepared incorporating the Cys to Cys constraint of peptide ~~cINSLa~~ cINSL3a. This compound, designated ~~cINSLb~~ cINSL3b, was a INSL3-based sequence, in which ~~Hisl2 form~~ His^{12} from the INSL3 sequence was replaced by Arg in an attempt to obtain an analogue of the putative relaxin receptor binding cassette ~~which if~~ absent in INSL3.--

Please cancel the present "SEQUENCE LISTING", pages 2-12, and insert therefor the accompanying paper copy of the Substitute Sequence Listing, page numbers 1 to 8, at the end of the application.